

Figure 1

2588 GA TCAATCGCAT TCATTTTAAG AAATTATACC TTITTAGTAC TTGCTGAAGA
2641 ATGATTTCAGG GTAAATCACA TACTTTGTTT AGAGAGGCGA GGGGTTTAAC CCGAGTCACC
2701 CAGCTGGTCT CATACATAGA CAGCACTTGT GAAGGATTGA ATGCAGGTTT CAGGTGGAGG
2761 GAAGACGTGG ACACCATCTC CACTGAGCCA TGCAGACATT TTAAAAAGCT ATACACAAAA
2821 TTGTGAGAAG ACATTGGCCA ACTCTTTCAA AGTCTTTCTT TTTCCACGTG CTTCTTATTT
2881 TAAGCGAAAT ATATTGTTTG TTTCTTCCTA AAAAAAAAAA 2890

Figure 2

1 CAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCTTCCTGATCCTGATC 60
61 TCTGTTCCGGCTGAGCTACCCACCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC 120
121 ATGCCCTCTGCAGGAACACTTCCTTGGGTTTCAGGGGATTATCTGTAATGCCAACAACCCC 180
1 M P S A G T L P W V Q G I I C N A N N P 20
181 TGTTTCCGTTACCCGACTCCTGGGGAGGCTCCCGAGTTGTTGGAAACTTTAACAATCC 240
21 C F R Y P T P G E A P G V V G N F N K S 40
241 ATTGTGGCTCGCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAAGACACC 300
41 I V A R L F S D A R R L L L Y S Q K D T 60
301 AGCATGAAGGACATGCGCAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 360
61 S M K D M R K V L R T L Q Q I K K S S S 80
361 AACTTGAAGCTTCAAGATTTCTTGGTGGACAATGAAACCTTCTCTGGGTTCTGTATCAC 420
81 N L K L Q D F L V D N E T F S G F L Y H 100
421 AACCTCTCTCTCCCAAAGTCTACTGTGGACAAGATGCTGAGGGCTGATGTCATTCTCCAC 480
101 N L S L P K S T V D K M L R A D V I L H 120
481 AAGGTATTTTTGCAAGGCTACCAGTTACATTGACAAGTCTGTGCAATGGATCAAAATCA 540
121 K V F L Q G Y Q L H L T S L C N G S K S 140
541 GAAGAGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCCTACCAAGGGAG 600
141 E E M I Q L G D Q E V S E L C G L P R E 160
601 AAAGTGGCTGCAGCAGAGCGAGTACTTCGTTCCAACATGGACATCCTGAAGCCAATCCTG 660
161 K L A A A E R V L R S N M D I L K P I L 180
661 AGAACAATAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAAACA 720
181 R T L N S T S P F P S K E L A E A T K T 200
721 TTGCTGCATAGTCTTGGGACTCTGGCCCAGGAGCTGTTTCAGCATGAGAAGCTGGAGTGAC 780
201 L L H S L G T L A Q E L F S M R S W S D 220
781 ATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC 840
221 M R Q E V M F L T N V N S S S S S T Q I 240
841 TACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGGGGCTGAAGATCAAG 900
241 Y Q A V S R I V C G H P E G G G L K I K 260
901 TCTCTCAACTGGTATGAGGACAACAATAAAGCCCTCTTTGGAGGCAATGGCACTGAG 960
261 S L N W Y E D N N Y K A L F G G N G T E 280

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961 GAAGATGCTGAAACCTTCTATGACAACCTCTACAACCTCCTTACTGCAATGATTGATGAAG 1020
281 E D A E T F Y D N S T T P Y C N D L M K 300
1021 AATTTGGAGTCTAGTCCTCTTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT 1080
301 N L E S S P L S R I I W K A L K P L L V 320
1081 GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCATGGCTGAGGTGAAC 1140
321 G K I L Y T P D T P A T R Q V M A E V N 340
1141 AAGACCTTCCAGGAACCTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAACCTCAGC 1200
341 K T F Q E L A V F H D L E G M W E E L S 360
1201 CCCAAGATCTGGACCTTCATGGAGAACAGCCAAGAAATGGACCTTGTCGGGATGCTGTTG 1260
361 P K I W T F M E N S Q E M D L V R M L L 380
1261 GACAGCAGGGACAATGACCACTTTTGGGAACAGCAGTTGGATGGCTTAGATTGGACAGCC 1320
381 D S R D N D H F W E Q Q L D G L D W T A 400
1321 CAAGACATCGTGGCGTTTTTGGCCAAGCACCCAGAGGATGTCCAGTCCAGTAATGGTTCT 1380
401 Q D I V A F L A K H P E D V Q S S N G S 420
1381 GTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCAGGCAATCCGGACCATATCTCGC 1440
421 V Y T W R E A F N E T N Q A I R T I S R 440
1441 TTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCCATAGCAACAGAAGTCTGGCTCATC 1500
441 F M E C V N L N K L E P I A T E V W L I 460
1501 AACAAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTGTTCACTGGA 1560
461 N K S M E L L D E R K F W A G I V F T G 480
1561 ATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT 1620
481 I T P G S I E L P H H V K Y K I R M D I 500
1621 GACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCCCTGGTCCTCGAGCT 1680
501 D N V E R T N K I K D G Y W D P G P R A 520
1681 GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG 1740
521 D P F E D M R Y V W G G F A Y L Q D V V 540
1741 GAGCAGGCAATCATCAGGGTGTGACGGGCACCGAGAAGAAAACCTGGTGTCTATATGCAA 1800
541 E Q A I I R V L T G T E K K T G V Y M Q 560
1801 CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGAGCCGGTCAATG 1860
561 Q M P Y P C Y V D D I F L R V M S R S M 580
1861 CCCCTCTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 1920
581 P L F M T L A W I Y S V A V I I K G I V 600
1921 TATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGCATC 1980
601 Y E K E A R L K E T M R I M G L D N S I 620
1981 CTCTGGTTTTAGCTGGTTCATTAGTAGCCTCATTCTCTTCTTGTGAGCGCTGGCCTGCTA 2040
621 L W F S W F I S S L I P L L V S A G L L 640
2041 GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTGTTGTC 2100
641 V V I L K L G N L L P Y S D P S V V F V 660
2101 TTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTCTTC 2160

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661 F L S V F A V V T I L Q C F L I S T L F 680
2161 TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC 2220
681 S R A N L A A A C G G I I Y F T L Y L P 700
2221 TACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC 2280
701 Y V L C V A W Q D Y V G F T L K I F A S 720
2281 CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGGAGCAG 2340
721 L L S P V A F G F G C E Y F A L F E E Q 740
2341 GGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCCTGTGGAGGAAGATGGCTTCAAT 2400
741 G I G V Q W D N L F E S P V E E D G F N 760
2401 CTCACCACTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG 2460
761 L T T S V S M M L F D T F L Y G V M T W 780
2461 TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATTCACAGGCCCTGGTATTTTCCTTGC 2520
781 Y I E A V F P G Q Y G I P R P W Y F P C 800
2521 ACCAAGTCTACTGTTTGGCGAGGAAAGTGATGAGAAGAGCCACCCTGGTTCCAACCAG 2580
801 T K S Y W F G E E S D E K S H P G S N Q 820
2581 AAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC 2640
821 K R I S E I C M E E E P T H L K L G V S 840
2641 ATTCAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCTGTGATGGCCTGGCA 2700
841 I Q N L V K V Y R D G M K V A V D G L A 860
2701 CTGAATTTTATGAGGGCCAGATCACCTCCTTCCTGGGCCACAATGGAGCGGGGAAGACG 2760
861 L N F Y E G Q I T S F L G H N G A G K T 880
2761 ACCACCATGTCAATCCTGACCGGGTGTTCCTCGGGCACCGCCTACATCCTG 2820
881 T T M S I L T G L F P P T S G T A Y I L 900
2821 GGAAAAGACATTGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGTCTGTCCCCAG 2880
901 G K D I R S E M S T I R Q N L G V C P Q 920
2881 CATAACGTGCTGTTTGACATGCTGACTGTGCAAGAACACATCTGGTTCTATGCCCGCTTG 2940
921 H N V L F D M L T V E E H I W F Y A R L 940
2941 AAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3000
941 K G L S E K H V K A E M E Q M A L D V G 960
3001 TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAGGTGGAATGCAGAGAAAG 3060
961 L P S S K L K S K T S Q L S G G M Q R K 980
3061 CTATCTGTGGCCTTGGCCTTTGTGCGGGGATCTAAGGTTGTCATTCTGGATGAACCCACA 3120
981 L S V A L A F V G G S K V V I L D E P T 1000
3121 GCTGGTGTGGACCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA 3180
1001 A G V D P Y S R R G I W E L L L K Y R Q 1020
3181 GGCCGCACCATTATTCTCTCTACACACCACATGGATGAAGCGGACGTCCTGGGGGACAGG 3240
1021 G R T I I L S T H H M D E A D V L G D R 1040
3241 ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC 3300
1041 I A I I S H G K L C C V G S S L F L K N 1060
3301 CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT 3360

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1061 Q L G T G Y Y L T L V K K D V E S S L S 1080
3361 TCCTGCAGAAACAGTAGTAGCACTGTGTACATACCTGAAAAAGGAGGACAGTGTTCCTCAG 3420
1081 S C R N S S S T V S Y L K K E D S V S Q 1100
3421 AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC 3480
1101 S S S D A G L G S D H E S D T L T I D V 1120
3481 TCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGGTGAAGACATA 3540
1121 S A I S N L I R K H V S E A R L V E D I 1140
3541 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTTGTGGAA 3600
1141 G H E L T Y V L P Y E A A K E G A F V E 1160
3601 CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3660
1161 L F H E I D D R L S D L G I S S Y G I S 1180
3661 GAGACGACCCTGGAAGAAATATTCCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG 3720
1181 E T T L E E I F L K V A E E S G V D A E 1200
3721 ACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCGGGGACAAGCAGAGC 3780
1201 T S D G T L P A R R N R R A F G D K Q S 1220
3781 TGTCTTCGCCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATTCTGACATAGACCCA 3840
1221 C L R P F T E D D A A D P N D S D I D P 1240
3841 GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGTCCTACCAGGTGAAA 3900
1241 E S R E T D L L S G M D G K G S Y Q V K 1260
3901 GGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCC 3960
1261 G W K L T Q Q Q F V A L L W K R L L I A 1280
3961 AGACGGAGTCGGAAGGATTTTTTGTCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGCATT 4020
1281 R R S R K G F F A Q I V L P A V F V C I 1300
4021 GCCCTTGTGTTTCAGCCTGATCGTGCCACCCTTTGGCAAGTACCCAGCCTGGAACCTTCAG 4080
1301 A L V F S L I V P P F G K Y P S L E L Q 1320
4081 CCCTGGATGTACAACGAACAGTACACATTTGTGAGCAATGATGCTCCTGAGGACACGGGA 4140
1321 P W M Y N E Q Y T F V S N D A P E D T G 1340
4141 ACCCTGGAACCTCTTAAACGCCCTCACCAAGACCCTGGCTTCGGGACCCGCTGTATGGAA 4200
1341 T L E L L N A L T K D P G F G T R C M E 1360
4201 GGAAACCCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCA 4260
1361 G N P I P D T P C Q A G E E E W T T A P 1380
4261 GTTCCCAGACCATCATGGACCTCTTCCAGAATGGGAAGTGGACAATGCAGAACCCTTCA 4320
1381 V P Q T I M D L F Q N G N W T M Q N P S 1400
4321 CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG 4380
1401 P A C Q C S S D K I K K M L P V C P P G 1420
4381 GCAGGGGGGCTGCCTCCTCCACAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTG 4440
1421 A G G L P P P Q R K Q N T A D I L Q D L 1440
4441 ACAGGAAGAAACATTTCCGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC 4500
1441 T G R N I S D Y L V K T Y V Q I I A K S 1460
4501 TTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTGAGT 4560

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1461 L K N K I W V N E F R Y G G F S L G V S 1480
4561 AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAA 4620
1481 N T Q A L P P S Q E V N D A T K Q M K K 1500
4621 CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT 4680
1501 H L K L A K D S S A D R F L N S L G R F 1520
4681 ATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT 4770
1521 M T G L D T R N N V K V W F N N K G W H 1540
4741 GCAATCAGCTCTTTCTGAATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAG 4800
1541 A I S S F L N V I N N A I L R A N L Q K 1560
4801 GGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAG 4860
1561 G E N P S H Y G I T A F N H P L N L T K 1580
4861 CAGCAGCTCTCAGAGGTGGCTCCGATGACCACATCAGTGGATGTCCTTGTGTCCATCTGT 4920
1581 Q Q L S E V A P M T T S V D V L V S I C 1600
4921 GTCATCTTTGCAATGTCCTTCGTCCAGCCAGCTTTGTCTGTTTCTGATCCAGGAGCGG 4980
1601 V I F A M S F V P A S F V V F L I Q E R 1620
4981 GTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTC 5040
1621 V S K A K H L Q F I S G V K P V I Y W L 1640
5041 TCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATC 5100
1641 S N F V W D M C N Y V V P A T L V I I I 1660
5101 TTCATCTGCTTCCAGCAGAAGTCCTATGTGTCTCCACCAATCTGCCTGTGCTAGCCCTT 5160
1661 F I C F Q Q K S Y V S S T N L P V L A L 1680
5161 CTACTTTTGTCTGTATGGGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTC 5220
1681 L L L L Y G W S I T P L M Y P A S F V F 1700
5221 AAGATCCCCAGCACAGCCTATGTGGTGCTCACCAGCGTGAACCTCTTCATTGGCATTAAAT 5280
1701 K I P S T A Y V V L T S V N L F I G I N 1720
5281 GGCAGCGTGGCCACCTTTGTGCTGGAGCTGTTACCGACAATAAGCTGAATAATATCAAT 5340
1721 G S V A T F V L E L F T D N K L N N I N 1740
5341 GATATCCTGAAGTCCGTGTTCTTGATCTTCCACATTTTGCCTGGGACGAGGGCTCATC 5400
1741 D I L K S V F L I F P H F C L G R G L I 1760
5401 GACATGGTGAAAAACCAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTT 5460
1761 D M V K N Q A M A D A L E R F G E N R F 1780
5461 GTGTCACCATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGG 5520
1781 V S P L S W D L V G R N L F A M A V E G 1800
5521 GTGGTGTCTTCTCCTCATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCAGACCT 5580
1801 V V F F L I T V L I Q Y R F F I R P R P 1820
5581 GTAAATGCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGGCGGGAAGACAG 5640
1821 V N A K L S P L N D E D E D V R R E R Q 1840
5641 AGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATA 5700
1841 R I L D G G G Q N D I L E I K E L T K I 1860
5701 TATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCTCCTGGTGAG 5760

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1861 Y R R K R K P A V D R I C V G I P P G E 1880
 5761 TGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTTTCAAGATGTTAACA 5820
 1881 C F G L L G V N G A G K S S T F K M L T 1900
 5821 GGAGATACCACTGTTACCAGAGGAGATGCTTTCCTTAACAGAAATAGTATCTTATCAAAC 5880
 1901 G D T T V T R G D A F L N R N S I L S N 1920
 5881 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG 5940
 1921 I H E V H Q N M G Y C P Q F D A I T E L 1940
 5941 TTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAA 6000
 1941 L T G R E H V E F F A L L R G V P E K E 1960
 6001 GTTGGCAAGGTTGGTGAGTGGGCGATTGCGAAACTGGGCCTCGTGAAGTATGGAGAAAAA 6060
 1961 V G K V G E W A I R K L G L V K Y G E K 1980
 6061 TATGCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6120
 1981 Y A G N Y S G G N K R K L S T A M A L I 2000
 6121 GGCGGGCCTCCTGTGGTGTCTTCTGGATGAACCCACCACAGGCATGGATCCCAAAGCCCGG 6180
 2001 G G P P V V F L D E P T T G M D P K A R 2020
 6181 CGGTTCTTGTGGAATTGTGCCCTAAGTGTGTCAAGGAGGGGAGATCAGTAGTGCTTACA 6240
 2021 R F L W N C A L S V V K E G R S V V L T 2040
 6241 TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA 6300
 2041 S H S M E E C E A L C T R M A I M V N G 2060
 6301 AGGTTCCAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGAGATGGTTATACA 6360
 2061 R F R C L G S V Q H L K N R F G D G Y T 2080
 6361 ATAGTTGTACGAATAGCAGGGTCCAACCCGACCTGAAGCCTGTCCAGGATTTCTTTGGA 6420
 2081 I V V R I A G S N P D L K P V Q D F F G 2100
 6421 CTTGCATTTCTCTGGAAGTGTTCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTT 6480
 2101 L A F P G S V P K E K H R N M L Q Y Q L 2120
 6481 CCATCTTCATTATCTTCTCTGGCCAGGATATTCAGCATCCTCTCCCAGAGCAAAAAGCGA 6540
 2121 P S S L S S L A R I F S I L S Q S K K R 2140
 6541 CTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACTTT 6600
 2141 L H I E D Y S V S Q T T L D Q V F V N F 2160
 6601 GCCAAGGACCAAGTGATGATGACCACTTAAAAGACCTCTCATTACACAAAACCAGACA 6660
 2161 A K D Q S D D D H L K D L S L H K N Q T 2180
 6661 GTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAAGAAAGCTAT 6720
 2181 V V D V A V L T S F L Q D E K V K E S Y 2200
 6721 GTATGAAGAATCCTGTTTCATACGGGGTGGCTGAAAGTAAAGAGGGACTAGACTTTCCTTT 6780
 2201 V *
 6781 GCACCATGTGAAGTGTGTGGAGAAAAGAGCCAGAAGTTGATGTGGGAAGAAGTAAACTG 6840
 6841 GATACTGTACTGATACTATTCAATGCAATGCAATTCAATG 6880

Figure 3

5' 1 GTACCCCCCT TGCCTGGTTG ATCCTCAGGG TTCTACTTAG AATGCCTCGA

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51 AAAGTCTTGG CTGGACACCC ATGCCCAGTC TTTCTGCAGG GTCCCATTTGG
101 GGTTAACCTT CTCATTTTCAT CCCATGTGAA CCAGGCCAGG CCCATCAGGG
151 TTTGGCAACC CCCTGATGCA GTGGTTGCTG CCAGGTGACA GGAGCAAGCC
201 TGCAGCTGCT GGGGGGCCAT GCAGAGACAG CCTGCCAGAG GGGAGACCAC
251 CTGGGGAGGC CAGAGCCGTG GAGACAGCAA GAGACCAGGG GCTGAGGACA
301 GAGTAGTACA GGTCTTTGGT CCCAGTAGTC CTGAAACCAC TGCACTCCGA
351 ACCTTTCTGT ACTTAGCTTA AGCCAGTTGG AGTTTCTGTC CTTTACAACC
401 AAGAGCCTTG ATAGGAATGG GGTCTGTGTC TACGCTACTG TTGGCTTCTT
451 TCCCGATCGG GCGCTGGAGG GGAACACAGC AGTGACTIONA GTGGGATGCT
501 TACTCGGTGC TGGGCATGCT AGAAAGTGCT TGCCATGCCT TATTTCCAC
551 GTGGTGGGGA TTTTGACCCC ACCTGTACAG ACAGATAAGT GAGGACCCTT
601 TTCACCTTAT CCTGCAACAG AAAATCCAGC AGCCAAAGCC AACAAGGGCC
651 CAGCATAGCA TCTTCCCTCT CTGACTTCAT CCTCACGCTC CACACACCAT
701 CCCCCTGGCC ATTCCAGCA GCCCAGTAAG CACTGCCTCA CACTTCCAGT
751 TCCGGACCAG CCAGGATGGC CAGGCTGGAT GGGGGCCATC CACCGGCTGA
801 AGCCAATTGC CTATTCTCGA GCTGAAGGTG AATCAATCCC GCATAAATCT
851 TCGGGCAGAG AACTNNGGTG GGGGGTAGAA GAGGGGGAAT GTCTAGAAGG
901 AAATTCTGGG GCACATTCTT GGAAGTGAGG AGGATGGATA TTGGACAGAA
951 ATTATGTCAT TGCAGGCACC CTCACTTGCC CTGGCCACAT GGACAGTTCC
1001 TCCCCGGCTG TGTTCCGNGC CTCTCTCGT GCTCCAGGGC CTGTCTGTTT
1051 CTGGAGCGAG ATGGGTCCCA GGGCTGGGCA CCAGTCCCCA TCTCCAGCCA
1101 TCAGGCACTT TCCTCTCTGT GTTTTGGCGT AAACACNTCC CTAGGTTTGT
1151 GGATCTGAAT CCTCTTCCCA ACACACTCAA GCTTTGCTGG GCCTCCCTGC
1201 AGTGTATGTT TAAGGCACCA CACAGCCTCC AAGGCCTGGC ACCCGGGCAG
1251 TGGCCACCTG GTAAACACAG CAGTCAGATT TCCTCATTTT AGCCAAGTGT
1301 AAAATCAAGG TAATGGATCT ACNCTTTTTT TTTTNTNTTT TTTCCAGGGG
1351 GNTNNTTTTT TTTTGAGACG GAGTCTCACT CTGTCANCCC CGGTCTGGAG
1401 TGCAGTGGCT CAATCTCGGC TCANCTGGCA AGCTCCGCCT CCCAGGTTCA
1451 TGCCATTCTC CTGCCTCAGC CTACATAGTA GCTGGGACTA CAGGTGCCCCG
1501 CCACCACACC TAGCTAATTT TTTGTATTTT TAGTAGAGAC GGGGTTTCAT
1551 CATGTTAGCC AGGATGGTCT CGATCTCCTG ACCTCCCAA GTGGTGGGAG
1601 TTACAGGTGT GAGCCACTGC GCNCCGGCTG GATGACTCTT GAGACAACAC
1651 CATTAGACA AAGGCAAGGC CTCCCACCTA AACTCATAAC CGTGTCTCCT
1701 TTCTCTCCTT CGATTTGAGC GGCTGAATTT GGTACAGTC ATCTGACCTG
1751 TGGGTGTGAA NGTCCACCTG CCTGGCATAA AAAGCTGTGC CTCCTTTCTA
1801 GGTGAGGAGA AAGAGAGAGA CCTGGCTCAT CTGAGGTGTG GTTGGGAGGG
1851 GGGACCCAGG TGTGCTGGAA ATGAAAAGAA ATGCATTCTT GTTTTTTCGT
1901 CCCAACATGC AAACAACCTGA ACAAAGCAT TAGGGCCTGA GACTGGGAGT
1951 AAAGAATTCC TTGTACCAT GGATACCAGG AAATGGCCCC ACTTATATAT
2001 AATAAGGGCT TTAGAGATGC TGGACCATCT GATATTCCAG CCTGGGGCCA
2051 CATGGGAGTG TGCCCTGGTG TTATTCCTTA TACAGTTCCA TGAACATGGC
2101 TCTGGAAACA CCTCTGTCTG CAGAAAATGA GGCTTTTCTT TTTTGTTCG

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2151 GGGGTGAACA GAGGGCAGAG GCCTGGGCAT CTTCCTCAG CACCCCTTTG
 2201 TAACCCAGCA CTTAGCACCA TGGCTGGCGC ACAGCAATGT CACATGTGTG
 2251 AGTGACACG ATGCCTCACT GCCAGGGGTC ACCCCACACC GGTGCTGTTG
 2301 GGGGCGTTGG AGTGGTTATC TCTTCTTTAG TCCTCAAGCT CCTACCTGGC
 2351 AGAGAGCTGC CCAACACCGT CGGGGTGGGG TGGGCGGGAA GGAAGAAGC
 2401 AGCAGCAAGA AAGAAGCCCC CTGGCCCTCA CTCTCCCTCC CTGGACGCCC
 2451 CCTCTTCGAC CCCATCACAC AGCCGCTTGA GCCTTGGAGN CAGTGGATTT
 2501 CCGAGCCTGG GAACCCCGG CGTCTGTCCC GGTGTCCCC GCAGCCTCAC
 2551 CCNCGTGCTG GCCCAGCCCC CGCGAGTTCG GGACCCGGGG TTTCCGGGGT
 2601 GGCAGGGGGT TCCCATGCCG CCTGCGAGGC CTCGGCTCGG GCCGCTCCCG
 2651 GAACCTGCAC TTCAGGGGTC CTGGTCCGCC GCCCCAGCA GGAGCAAAAC
 2701 AAGAGCACGC GCACCTGCCG GCCCGCCCCG CCCCTTGGTG CCGGCCAATC
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 2801 CCCAGCCGGA GCCCAAGCGC AGCCCGCACC CCGCGCAGCG GCTGAGCCGG
 2851 GAGCCAGCGC AGCCTCGGCC CCGCAGCTCA AGCCTCGTCC CCGCCGCCNG
 2901 CCGCCGCACG CCGCCGCCG CGCCCCGGG GCATGGGCTGT CTGATGGCCG

EXON1/INTRON 1

2951 CTTTCTCGGT CGGCACCGCC ATGGTGAGTG AGCGCATCCT TCGTCCGCCG
 3001 GGAACGGTTT TATTTTCAAG GAGAGCAGGA AACACACAAA GACTCGCAAG
 3051 CTCGACCTGA CACCCCTCCC AGGAGCGCGT CCTCTGGGGC GCTGACCCAG
 3101 GGGCACCTTA GAGTGGCGCC CGGCTCCGAT CGCTGCCCT NNCCCCTCCG
 3151 CCAGGGCCAC CTGGGAGCCT CGGGGATGCC CCTTGCACCG GCAGAGNGCA
 3201 CGGACTAGGT GGAGGGGNCC GGGATTGGGG CGGGGGGCAG NCAGTTGCCC
 3251 TACAAGTTGG ACCGATGGCC TTGACCTGAT GGCTTCTGGG CGGGGGGCGT
 3301 GGGGAGCTGG GGACCCGGAG CGCACTGGGG ACTGGGGAGG GGCCGCAGCT
 3351 TGGGCCGGAG GGAAGAGGGG ACTTGAAGAA GGGGAGCCCC GCGCGCGCGG
 3401 CTGTGGGCTT GGGGACCGGG GACTTCTCGC GCCATCCCCA GGAACGCCAG
 3451 GCAAGGTCTG GGGAACAAAA GAGGAAGCTG CCCCAGAGA GCCGGAGCTC
 3501 GACTGNACTC CC 3'

Figure 4

5'

1 CTTGGTGCCG CATGCATCGT GGTGCTCATC TTTCTGGCCT TCCAGCAGAG
 51 GGCATATGTG GCCCCTGCCA ACCTGCCTGC TCTCCTGCTG TTGCTACTAC
 101 TGTATGGCTG GTCGATCACA CCGCTCATGT ACCCAGCCTC CTTCTTCTTC
 151 TCCGTGCCCC GCACAGCCTA TGTGGTGCTC ACCTGCATAA ACCTCTTTAT
 201 TGGCATCAAT GGAAGCATGG CCACCTTTGT GCTTGAGCTC TTCTCTGATC
 251 AGAAGCTGCA GGAGGTGAGC CGGATCTTGA AACAGGTCTT CTTATCTTC
 301 CCCACTTCTG CTTGGGCCGG GGGCTTATTG ACATGGTGCG GNAACCAGGC
 351 CATGGCTGAT GCCTTTGANC CCTTGGGAAA AAGGCAGTTC AAGTACCCTG

401 NCTTGGAAGG TGGCGGAAGA ACCTTTTGGC ATGGGAACAG GGCCCCTTTT
451 CCTTCTCTTC ACACTANTGT TCAAGCACCG AAGCCAACTC NTGCCACAAG
501 CCCAGGTAAG GTCTCTGCCA CTCCTGGAGA GAGACGAGGA TGTAGCCCGT
551 GAACGGGAGC GGGTGGTCCA AGGAGCCACC CAGGGGGATG TGTTGGTGCT
601 GAGGAACTTG ACCAAGGTAT ACCGTGGGCA GAGGATGCCA GCTGTTGACC
651 GCTTGTGCCT GGGGATTCCC CCTGGTGAGT GTTTTGGGCT GCTGGGTGTG
701 AACGGAGCAG GGAAGACGTC CACGTTTCGC ATGGTGACGG GGGACACATT
751 GGCCAGCAGG GGCGAGGCTG TGCTGGCAGG CCACAGCGGG CCCGGGAACC
801 CAGTGTGCGC ACCTCNAGGG CAGGCNCAGC GTGGCCCGGG AACCCAGTGC
851 TGCGCACCTA AGCATGGGAT ACTGCCCTNA ATCCGATGCC ATCTTTGAGC
901 TGCTGACGGG CCGCGAGCAC CTGGAGCTGC TTGCGCGCCT GCGCGGTGTC
951 CCGGAGGCCC AGGTTGCCCC NACCGNTGGC TCGGGCCTGG CGCGTCTGGG
1001 ACTCTCATGG TACGCAGACC GGCCTGCAGG CACCTACAGG AACCTGCCCC
1051 GGCGGCCGCT CGAGCCCNNTA NNTGAAGTA 3'

Figure 4b

...CTCCTGCCAC AGTTAGTGAG GTCTATGGAG AGGGTGGCAG GGGCCAAGGA
CCTACTTTAA GCCACAGAT ATTCTGTCCC CAGGCCCAGG GTGAGGTCTC...

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Figure 5

CDNA-sequences of lipid sensitive Genes:

ABCB9, ABCA6, ABCC4, ABCA1, ABCD2, ABCB1, ABCB4, ABCC2, ABCD1, ABCC1, ABCB6, ABCB11, ABCG2, ABCC5, ABCA5, ABCG1, ABCA3

ABCB9 GENBANK:U66676

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AGGGCGCCCAGCTGTCAGGTGGCCAGAAGCAGCGGGTGGCCATGGCCGNGGCTCTGGTG
GGAACCCCCCAGTCCTCATCCTGGATGAAGCCACCAGCGCTTTGGATGCCGAGAGCGAGT
ATCTGATCCAGCAGGCCATCCATGGCAACCTGTGAGAAGCACACGGTACTCATCATCGCG
CACCGGCTGAGCACCGTGGAGCACGCGCACCTCATTGTGGTGCTGGACAAGGGCCGCGTA
GTGCAGCAGGGCACCCACCAGCAGCTTGCTTGCCCCAGGGCGGGCTTTTACGGCAAGCTN
GTTGCAGCGGCAGATGTGGGGTTTCAAGGCCGAGACTTCACAGCTGGCCACAACGAGCC
TGTAAGCAACGGGTCAAGGCCTGATGGGGGGCCCTCCTTCGCCCCGGTGGCAGAGGAC
CCGGTGCTGCTGGCAGATGTGCCACGGAGGTTTCCAGCTGCCCTACCGAGCCCAGGC
CTGCAGCACTGAAAGACGACCTGCCATGTCCCATGATCACCGCTTNTGCAATCTTGCCCC
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ACACGAAACCTCAACTGGGGGAGTGAGGAGCTGGCCAGGTCTGGAGGGGCTCAGGTGCC
CCCAGCCCCGGCACCCAGCTTTGCCCCCTCGTCAATCAACCCCTGGCTGGCAGCCGCCCTC
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ABCA6 GENBANK:U66680

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CCCATAACCTGGCTGAGGCGGAAGCCTTGTGTGACCGTGTGGCCATCATGGTGTCTGGAA
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TAGAGCTAAAAGTGAAGGAAACGTCTCAAGTGACTTTGGTCCACACTGAGATTCTGAAGC

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ABCC4 GENBANK:U66682

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ABCA1 Acc.Nr.: AJ012376 GENBANK:HSA012376

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ABCD2 Acc.Nr.: AJ000327 GENBANK:HSALDR

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ABCB1 Acc.Nr. M14758 GENBANK:HUMMDR1

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ABCB4 Acc. Nr.: M23234 GENBANK:HUMMDR3

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ABCC2 Acc.Nr.: U49248 GENBANK:HSU49248

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ABCD1 Acc.Nr.: Z21876 GENBANK:HSXLALDA

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ABCC5 GENBANK: AF104942

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ABCA5 Acc.Nr.: AF000148 GENBANK: HSAF000148

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CGGTGCCGGCTATCACATGACGCTGGTGAAGGAGCCGCACTGCAACCCGGAAGACATCTC
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GTCTTTTCATCCTTCCCAGAGAGAGCACGCACAGGTTTGAAGGTCTCTTTGCTAAACTGGA
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AGTCTTCTTCGGGTGCGGAAGCTGGTGGACAGCAGTATGGACATCCAGGCCATCCAGCT
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CTGTGGGGCCATGGACCCCTCCGACGGCATTTGGAGCCCTCATCGAGGAGGAGCGCACCGC
TGTCAGCTCAACACTGGGCTCGCCCTGCACTGCCAGCAATTCTGGGGCATGTTCTCTGAA

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GAAGGCCGCATACAGCTGGCGCGAGTGGAATGGTGGCGGCACAGGTCCTGGTGCCTCT
GACCTGCGTCACCTGGCCCTCCTGGCCATCAACTACTCCTCGGAGCTCTTCGACGACCC
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CCTGCAGCCGCCCCACCGCAGAGGAGGGGCGATGAGGGGTGGCGGCTGTCTCGCCATCAGG
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GAATGGACGAGTGCAGCCCAGCCCTCATGCCCAGGATCAGCATGCGCATCTCCATGTCTG
CATACTCTGGAGTTCACTTTCCCAGAGCTGGGGCAGGCCGGGCAGTCTGCGGGCAAGCTC
CGGGGTCTCTGGGTGGAGAGCTGACCCAGGAAGGGCTGCAGCTGAGCTGGGGGTGAATT
TCTCCAGGCACTCCCTGGAGAGAGGACCCAGTGACTTGTCCAAGTTTACACACGACACTA
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TGCTGGGGTCTTAGCGTCCAGCGCAGCCCGGGGCATCCTGGAGGCTCTGCTCCCTTAGG
GCATGGTAGTCACCGGAAGCCGGGCACCGTCCCACAGCATCTCCTAGAAGCAGCCGGCA
CAGGAGGGAAGGTGGCCAGGCTCGAAGCAGTCTCTGTTTCCAGCACTGCACCCTCAGGAA
GTCGCCCCGCCCCAGGACACGCAGGGACCACCCTAAGGGCTGGGTGGCTGTCTCAAGGACA
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AAAAA

Fragment 640918

1 GAGATCCTGAGGCTTTTCCCCAGGCTGCTCAGCAGGAAAGGTTCTCCTCCCTGATGGTC
61 TATAAGTTGCCTGTTGAGGATGTGCGACCTTTATCACAGGCTTTCTTCAAATTAGAGATA
121 GTTAAACAGAGTTTCGACCTGGAGGAGTACAGCCTCTCACAGTCTACCCTGGAGCAGGTT
181 TTCCTGGAGCTCTCCAAGGAGCAGGAGCTGGGTGATCTTGAAGAGGACTTTGATCCCTCG
241 GTGAAGTGAAACTCCTCCTGCAGGAAGAGCCTTAAAGCTCCAAATACCCTATATCTTTC
301 TTTAATCCTGTGACTCTTTTAAAGATAATATTTTATAGCCTTAATATGCCTTATATCAGA
361 GGTGGTACAAAATGCATTTGAAACTCATGCAATAATTATC

Fragment 698739

1 GCTCTCCACACAGAGATTTTGAAGCTTTTCCCACAGGCTGCTTGGCAGGAAAGATATTCC
61 TCTTTAATGGCGTATAAGTTACCTGTGGAGGATGTCCACCCTCTATCTCGGGCTTTTTC
121 AAGTTAGAGGCGATGAAACAGACCTTCAACCTGGAGGAATACAGCCTCTCTCAGGCTACC
181 TTGGAGCAGGTATTCTTAGAACTCTGTAAAGAGCAGGAGCTGGGAAATGTTGATGATAAA
241 ATTGATACAACAGTTGAATGGAACTTCTCCACAGGAAGACCCTTAAATGAAGAACCT
301 CCTAACATTCAATTTTAGGTCCTACTACATTGTTAGTTTCCATAATTCTACAAGAAATGTT
361 TCCTTTTACTTCAGTTAACAAAAGAAAACATTTAATAAACATTCAATAATGATTACAGTT
421 TTCATTTTAAAAATTTAGGATGAAGGAAACAAGGAAATATAGGGAAAAGTAGTAGACAA
481 AATTAACAAAATCAGACATGTTATTTCATCCCCAACATGGGTCTATTTTGTGCTTAAAAAT
541 AATTTAAAAATCATACAATATTAGGTTGGTTATCG

Fragment 990006

1 GTGGAAGATGTGCAACCTTTAGCCCAAGCTTTCTTCAAATTAGAGAAGGTTAAACAGAGC
61 TTTGACCTAGAGGAGTACAGCCTCTCACAGTCTACCCTGGAGCAGGTTTTCTGGAGCTC
121 TCCAAGGAGCAGGAGCTGGGTGATTTTGAGGAGGATTTTGATCCCTCAGTGAAGTGAAG

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181 CTCCTCCCCCAGGAAGAGCCTTAAAACCCCAAATTCTGTGTTCCCTGTTTAAACCCGTGGT
241 TTTTTTTTAAATACATTTATTTTATAGCAGCAATGTTCTATTTTATAGAACTATATTATA

Fragment 1133530

1 TTTTCAGTTG CATGTAATAC CAAGAAATCG AATTGTTTTC CGGTTCTTAT
51 GGGGAATTGTT AGCAATGCCC TTATTGGAAT TTTTAACTTC ACAGAGCTTA
101 TTCAAATGGA GAGCACCTTA TTTTTCGTG ATGACATAGT GCTGGATCTT
151 GGTTTTATAG ATGGGTCCAT ATTTTGTG TTGATCACA ACTGCATTTC
201 TCCTTATATT GGCATAAGCA GCATCAGTGA TTATT

Fragment 1125168

CTGGATT

TGCTCTGCGG CAAGACCCGC GCCACCAGCG GCAGTATCCA GTTCGACGGC
CAGGAACTGA CCAAATGCG CGAATACAAC ATCGTGCGGG CCGGGGTAGG
GCGCAAGTTT CAGAACCCGT CGATCTACGA AAACCTCACG GTGTTTGAAA
ACCTTGAGAT GTCTTATCCG GCTGGGCGCA AGGTCTGGGG TCGCTGTTT
TTCAAGCGCA ATGCCAGGT GGTGGCGCGG GTCGAG

Fragment 1203215

1 ATCGCCGATA TCTCCCCTTC GGGCTGCGGC AAGAGCACCT TCCTGAAAGT
51 GCTCGCCGGG TTCTATGCCC TGGACACCGG GCGCTTCAGG ATCAACGGCC
101 AGGCGATGCG GCATTTCTGGT TTGCGCTCGT ACCGCCAGAG CGTGGCCTAT
151 GTCACGGCCC ACGACGAGAT CATCGCCGGG ACGGTGATCG AGAACATCCT
201 GATGGACAGC GACCCGCTGG ACGGCACGGG TTTGCAGAGC TGTGTCGAGC
251 AGGCCGGGTT GCTGGAAAGC ATCCTGAAAC TGAGCAATGG CTTCAATACC
301 TTGCTCGGAC CCATGGGCGT GCAATTGTCC TCGGGCCAGA AGCAACGCCT
351 GTTGATCGCC CGGGGTCGAC GC

Fragment 168043

1 AAAACCAAAG ATTCTCCTGG AGTTTTCTCT AAACCTGGGTG TTCTCCTGAG
51 GAGAGTTGAC AAGAACTTG GTGAGAAATA AGCTGGCAGT GATTACGCGT
101 CTCCTTCAGA ATCTGATCAT GGGTTTGTTT CTCCTTTTCT TCGTTCTGCG
151 GGTCCGAAGC AATGTGCTAA AGGGTGCTAT CCAGGACCGC GTAGGTCTCC
201 TTTACCAGTT TGTGGGCGCC ACCCCGTACA CAGGCATGCT GAACGCTGTG
251 AATCTGTTTC CCGTGCTGCG AGCTGTCAGC A

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1 ATGGCCGTGA CGCTGGAGGA CGGGGCGGAA CCCCCTGTGC TGACCACGCA
51 CCTGAAGAAG GTGGAGAACC ACATCACTGA AGCCCAGCGC TTCTCCACC
101 TGCCCAAGCG CTCAGCCGTG GACATCGAGT TCGTGGAGCT GTCCTATTCC
151 GTGCGGGAGG GGCCCTGCTG GCGCAAAAGG GGTATAAGA CCCTTCTCAA
201 GTGCCTCTCA GGTAAATTCT GCCGCCGGGA GCTGATTGGC ATCATGGGCC
251 CCTCAGGGGC TGGCAAGTCT ACATTCATGA ACATCTTGGC AGGATACAGG
301 GAGTCTGGAA TGAAGGGGCA GATCCTGGTT AATGGAAGGC CACGGGAGCT

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351 GAGGACCTTC CGCAAGATGT CCTGCTACAT CATGCAAGAT GACATGCTGC
401 TGCCGCACCT CACGGTGTTG GAAGCCATGA TGGTCTCTGC TAACCTGAAT
451 CTTACTGAGA ATCCCGATGT GAAAAACGAT CTCGTGACAG AGATCCTGAC
501 GGCACCTGGG CTGATGTCGT GCTCCACAC GAGGACAGCC CTGCTCTCTG
551 GCGGGCAGAG GAAGCGTCTG GCCATCGCCC TGGAGCTGGT CAACAACCCG
601 CCTGTCTATGT TCTTTGATGA GCCCACCAGT GGTCTGGATA GCGCCTCTTG
651 TTTCCAAGTG GTGTCCCTCA TGAAGTCCCT GGCACAGGGG GGCCGTACCA
701 TCATCTGCAC CATCCACCAG CCCAGTGCCA AGCTCTTTGA GATGTTTGAC
751 AAGCTCTACA TCCTGAGCCA GGGTCAGTGC ATCTTCAAAG GCGTGGTCAC
801 CAACCTGATC CCCTATCTAA AGGGACTCGG CTTGCATTGC CCCACCTACC
851 ACAACCCGGC TGAATTCACT GAGTGGGGGT CTGTTGCCTC TGGCGAGTAT
901 GGACACCTGA ACCCCATGTT GTTCAGGGCT GTGCAGAATG GGCTGTGCGC
951 TATGGCTGAG AAGAAGAGCA GCCCTGAGAA GAACGAGGTC CCTGCCCAT
1001 GCCCTCCTTG TCCTCCGGAA GTGGATCCCA TTGAAAGCCA CACCTTTGCC
1051 ACCAGCACCC TCACACAGTT CTGCATCCTC TTCAAGAGGA CCTTCCTGTC
1101 CATCCTCAGG GACACGGTCC TGACCCACCT ACGGTTTCATG TCCCACGTGG
1151 TTATTGGCGT GCTCATCGGC CTCCTCTACC TGCATATTGG CGACGATGCC
1201 AGCAAGGTCT TCAACAACAC CGGCTGCCTC TTCTTCTCCA TGCTGTTCCCT
1251 CATGTTTCGCC GCCCTCATGC CAACTGTGCT CACCTTCCCC TTAGAGATGG
1301 CGGTCTTCAT GAGGGAGCAC CTCAACTACT GGTACAGCCT CAAAGCGTAT
1351 TACCTGGCCA AGACCATGGC TGACGTGCCC TTTCAGGTGG TGTGTCCGGT
1401 GGTCTACTGC AGCATTGTGT ACTGGATGAA CGGCCAGCCC GCTGAGACCA
1451 GCCGCTTCCT GCTCTTCTCA GCCCTGGCCA CCGCCACCGC CTTGGTGGCC
1501 CAATCTTTGG GGCTGCTGAT CGGAGCTGCT TCCAACCTCC TACAGGTGGC
1551 CACTTTTGTG GGCCCAGTTA CCGCCATCCC TGTCTCTTG TTCTCCGGCT
1601 TCTTTGTGAG CTTCAAGACC ATCCCCACTT ACCTGCAATG GAGCTCCTAT
1651 CTCTCCTATG TCAGGTATGG CTTTGAGGGT GTGATCCTGA CGATCTATGG
1701 CATGGAGCGA GGAGACCTGA CATGTTTAGA GGAACGCTGC CCGTTCGGG
1751 AGCCACAGAG CATCCTCCGA GCGCTGGATG TGGAGGATGC CAAGCTCTAC
1801 ATGGACTTCC TGGTCTTGGG CATCTTCTTC CTAGCCCTGC GGCTGCTGGC
1851 CTACCTTGTG CTGCGTTACC GGGTCAAGTC AGAGAGATAG AGGCTTGCCC
1901 CAGCCTGTAC CCCAGCCCCC GCAGCAGGAA GCCCCCAGTC CCAGCCCCCTT
1951 GGGACTGTTT TANCTCTATA CACTTGGGCA CTGGTTCCTG GCGGGGCTAT
2001 CCTCTCCTCC CTTGGCTCCT CCACAGGCTG GCTGTGCGAC TGCGCTCCCA
2051 GCCTGGGCTC TGGGAGTGGG GGCTCCAACC CTCCCCACTA TGCCAGGAG
2101 TCTTCCCAAG TTGATGCGGT TTGTAGCTTC CTCCCTACTC TCTCCAACAC
2151 CTGCATGCAA AGACTACTGG GAGGCTGCTG CCTCCTTCCT GCCCATGGCA
2201 CCCTCCTCTG CTGTCTGCCT GGGAGCCCTA GGCTCTCTAT GGCCCCACTT
2251 ACAACTGA

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Fragment 20237

1 TTTAAGGATT TCAGCCTTTC CATTCCGTCA GGATCTGTCA CGGCACTGGT TGGCCCAAGT
61 GGTTC TGGCA AATCAACAGT GCTTTCACCTC CTGCTGAGGT TGTACGACCC TGCTTCTGGA
121 ACTATTAGTC TTGATGGCCA TGACAATCCG TCAGCTAAAC CCAGTGTGTG GCTGAGATCC
181 AAAATTGGGA CAGTCAGTCA GGAACCCATT TTGTTTTCTT GCTCTATTGC TGAGAACATT
241 GCTTATGGTG CTGATGACCC TTCCTCTGTG ACCGCTGAGG AAATCCAGAG AGTGGCTGAA
301 GTGGCCAATG CAGTGGCTTC TCCGGAATTT CCCCCAAGGT TCAACACTGT GGTGGAGAA
361 AAGGGTGTTT TCCTCTCAGG TGGGCAGAAA CAGCGGATTG CGATTGCCCC TGCTCTGCTA
421 AAGAATCCCA AAATTCTTCT CCTAGATGAA GCAACCAGTG CGCTGGATGC CGAAAATGAG
481 TACCTTGTTT AAGAAGCTCT AGATCGCCTG ATGGATGGAA GAACGGTGTT AGTTATTGCC
541 CATAGCCTGT CCACCATTAA GAATGCTAAT ATGGTTGCTG TTCTTGACCA AGGAAAAATT
601 ACTGAATATG GAAAACATGA AGAGCTGCTT TCAAAACCAA ATGGGATATA CAGAAAACCTA
661 ATGAACAAAC AAAGTTTTAT TTCAGCATAA GGAAGCAATT ACTGGTAAAC AATATGAGAC
721 TTTAATGCAA AACAGTGTTG CGAAAAAAA CTCAGAGACT ATGAAATACA TAAACCATAT
781 ATCAAGTTAT TTGAAAAATA CCTATTTTTT CCAAAGTGTG

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102250 5599260